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Reviewer: Anne Corrigan

Timestamp: Fri Nov 02 14:26:43 EDT 2007

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Application No: 10592944

Version No: 1.0

**Input Set:****Output Set:****Started:** 2007-10-18 13:49:33.374**Finished:** 2007-10-18 13:49:34.851**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 477 ms**Total Warnings:** 25**Total Errors:** 0**No. of SeqIDs Defined:** 26**Actual SeqID Count:** 26

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**Input Set:**

**Output Set:**

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**No. of SeqIDs Defined:** 26  
**Actual SeqID Count:** 26

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

# SEQUENCE LISTING

<110> BOUGERET, CECILE  
ZARZOV, PATRICK  
BRIAND, JEAN-FRANCOIS  
THOMAS, DOMINIQUE

<120> METHOD FOR SCREENING AGENTS MODULATING I-KAPPA B-ALPHA  
PROTEIN UBIQUITINATION AND MEANS FOR CARRYING OUT SAID  
METHOD

<130> 0510-1149

<140> 10592944

<141> 2007-10-18

<150> PCT/FR05/050165

<151> 2005-03-15

<150> FR 04 50528

<151> 2004-03-16

<160> 26

<170> PatentIn Ver. 3.3

<210> 1

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
construct

<400> 1

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agcccacctc caaaaaagaa gagaaagggtc gaattggggtg gatccatgtt ccaggcggcc 780
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<210> 2

<211> 572

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
construct

<400> 2

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
  1              5              10             15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
      20              25              30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
      35              40              45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
      50              55              60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
      65              70              75             80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
      85              90              95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
      100             105             110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
      115             120             125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
      130             135             140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
      145             150             155             160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
      165             170             175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
      180             185             190

```

Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	195	200	205	
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	210	215	220	
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Leu	Gln	225	230	235	240
Ser	Pro	Pro	Pro	Lys	Lys	Lys	Arg	Lys	Val	Glu	Leu	Gly	Gly	Ser	Met	245	250	255	
Phe	Gln	Ala	Ala	Glu	Arg	Pro	Gln	Glu	Trp	Ala	Met	Glu	Gly	Pro	Arg	260	265	270	
Asp	Gly	Leu	Lys	Lys	Glu	Arg	Leu	Leu	Asp	Asp	Arg	His	Asp	Ser	Gly	275	280	285	
Leu	Asp	Ser	Met	Lys	Asp	Glu	Glu	Tyr	Glu	Gln	Met	Val	Lys	Glu	Leu	290	295	300	
Gln	Glu	Ile	Arg	Leu	Glu	Pro	Gln	Glu	Val	Pro	Arg	Gly	Ser	Glu	Pro	305	310	315	320
Trp	Lys	Gln	Gln	Leu	Thr	Glu	Asp	Gly	Asp	Ser	Phe	Leu	His	Leu	Ala	325	330	335	
Ile	Ile	His	Glu	Glu	Lys	Ala	Leu	Thr	Met	Glu	Val	Ile	Arg	Gln	Val	340	345	350	
Lys	Gly	Asp	Leu	Ala	Phe	Leu	Asn	Phe	Gln	Asn	Asn	Leu	Gln	Gln	Thr	355	360	365	
Pro	Leu	His	Leu	Ala	Val	Ile	Thr	Asn	Gln	Pro	Glu	Ile	Ala	Glu	Ala	370	375	380	
Leu	Leu	Gly	Ala	Gly	Cys	Asp	Pro	Glu	Leu	Arg	Asp	Phe	Arg	Gly	Asn	385	390	395	400
Thr	Pro	Leu	His	Leu	Ala	Cys	Glu	Gln	Gly	Cys	Leu	Ala	Ser	Val	Gly	405	410	415	
Val	Leu	Thr	Gln	Ser	Cys	Thr	Thr	Pro	His	Leu	His	Ser	Ile	Leu	Lys	420	425	430	
Ala	Thr	Asn	Tyr	Asn	Gly	His	Thr	Cys	Leu	His	Leu	Ala	Ser	Ile	His	435	440	445	
Gly	Tyr	Leu	Gly	Ile	Val	Glu	Leu	Leu	Val	Ser	Leu	Gly	Ala	Asp	Val	450	455	460	
Asn	Ala	Gln	Glu	Pro	Cys	Asn	Gly	Arg	Thr	Ala	Leu	His	Leu	Ala	Val	465	470	475	480
Asp	Leu	Gln	Asn	Pro	Asp	Leu	Val	Ser	Leu	Leu	Leu	Lys	Cys	Gly	Ala	485	490	495	

Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu Thr  
500 505 510

Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu Thr  
515 520 525

Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser Tyr  
530 535 540

Asp Thr Glu Ser Glu Phe Thr Glu Phe Thr Glu Asp Glu Leu Pro Tyr  
545 550 555 560

Asp Asp Cys Val Phe Gly Gly Gln Arg Leu Thr Leu  
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<210> 3

<211> 2583

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
construct

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<210> 4

<211> 860

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
construct

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Met Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
          20             25             30

```

```

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
    35             40             45

```

```

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50             55             60

```

```

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
    65             70             75             80

```

```

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
          85             90             95

```

```

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
    100             105             110

```

```

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
    115             120             125

```

```

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130             135             140

```

```

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
    145             150             155             160

```

```

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
          165             170             175

```



Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	180	185	190
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	195	200	205
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	210	215	220
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Leu	Gln	225	230	235
Ser	Pro	Pro	Pro	Lys	Lys	Lys	Arg	Lys	Val	Glu	Leu	Gly	Gly	Ser	Met	245	250	255
Asp	Pro	Ala	Glu	Ala	Val	Leu	Gln	Glu	Lys	Ala	Leu	Lys	Phe	Met	Cys	260	265	270
Ser	Met	Pro	Arg	Ser	Leu	Trp	Leu	Gly	Cys	Ser	Ser	Leu	Ala	Asp	Ser	275	280	285
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Ala	Phe	Gln	Asn	Ser	Ser	Glu	Arg	Glu	Asp	Cys	Asn	Asn	Gly	Glu	Pro	305	310	315
Pro	Arg	Lys	Ile	Ile	Pro	Glu	Lys	Asn	Ser	Leu	Arg	Gln	Thr	Tyr	Asn	325	330	335
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Tyr	Glu	Lys	Glu	Lys	Glu	Leu	Cys	Val	Lys	Tyr	Phe	Glu	Gln	Trp	Ser	385	390	395
Glu	Ser	Asp	Gln	Val	Glu	Phe	Val	Glu	His	Leu	Ile	Ser	Gln	Met	Cys	405	410	415
His	Tyr	Gln	His	Gly	His	Ile	Asn	Ser	Tyr	Leu	Lys	Pro	Met	Leu	Gln	420	425	430
Arg	Asp	Phe	Ile	Thr	Ala	Leu	Pro	Ala	Arg	Gly	Leu	Asp	His	Ile	Ala	435	440	445
Glu	Asn	Ile	Leu	Ser	Tyr	Leu	Asp	Ala	Lys	Ser	Leu	Cys	Ala	Ala	Glu	450	455	460
Leu	Val	Cys	Lys	Glu	Trp	Tyr	Arg	Val	Thr	Ser	Asp	Gly	Met	Leu	Trp	465	470	475
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Lys Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly  
 485 490 495

Leu Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro  
 500 505 510

Pro Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro  
 515 520 525

Lys Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly  
 530 535 540

Arg His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly  
 545 550 555 560

Val Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg  
 565 570 575

Asp Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg  
 580 585 590

Ile Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu  
 595 600 605

Arg Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp  
 610 615 620

Val Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala  
 625 630 635 640

Val Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys  
 645 650 655

Asp Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr  
 660 665 670

Leu Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp  
 675 680 685

Phe Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys  
 690 695 700

Val Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His  
 705 710 715 720

Lys Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser  
 725 730 735

Gly Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala  
 740 745 750

Cys Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg  
 755 760 765

Phe Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys  
 770 775 780

Val Trp Asp Leu Val Ala